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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.76512 Seconds

(without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613b-21

Perfect score: 605  
Sequence: 1 MGNMATEFOOKHIIINFPILCN.....ICVKGCEQNPVHFAGIGRCP 111

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query length	DB ID	Description
1	585.5	36.8	111.1	RNPO_RANCA P11916 rana catesb
2	451	74.5	111.1	LECS_RANCA P18839 rana japoni
3	370	31.2	111.1	RNPL_RANCA P14626 rana catesb
4	273.5	15.2	104	RN30_RANPI P22069 rana pipien
5	154.5	25.5	145	ANG3_MOUSE P97802 mus musculu
6	149.5	24.7	145	ANGR_MOUSE O64438 mus musculu
7	136.5	22.6	145	ANGI_MOUSE P21570 mus musculu
8	133.5	21.7	124	RNP_BALAC P00673 balaenopter
9	129.5	21.4	124	RNP_PIG P00671 sus scrofa
10	129.5	21.4	167	RNBR_BOVIN P39873 bos taurus
11	127.5	21.1	119	RNP_IGUIG P80287 iguana igua
12	124.5	20.6	151	RNBR_CAPCA P79351 capreolus c
13	123.5	20.4	123	ANG2_BOVIN P80929 bos taurus
14	123.5	20.4	141	RNBR_GIRCA Q23542 giraffa cam
15	123.5	20.4	151	RNBR_AXIRA P87350 axis porcin
16	123	20.3	146	ANGI_MIOTA O8wn65 miotiphecus
17	120	19.8	146	ANGI_SAISC O8wn60 saimiri sci
18	120	19.8	147	ANGI_CERAE O8wn66 cercoptilhec
19	120	19.8	147	ANGI_PONYA Q25543 ponyo pygma
20	119.5	19.8	143	RNBR_SHEEP O25543 ovis aries
21	119	19.7	122	RNP_MACRU P00686 macropus ru
22	118.5	19.6	123	ANGI_PIG P31346 sus scrofa
23	118.5	19.6	124	RNP_ANTAM P00668 antilocapra
24	118	19.5	146	ANGI_AOTR O8wn61 aotus trivi
25	117	19.3	146	ANGI_SAGOE O8wn62 saguinus oe
26	116.5	19.3	128	RNP_MYOCO P00676 myocastor c
27	116.5	19.3	149	RNP_MOUSE P00683 mus musculu
28	115	19.0	146	ANGI_MACMU O8wn63 macaca mula
29	114.5	18.9	128	RNPB_CAVIO P00679 cavia porce
30	114	18.8	148	ANGI_BOVIN P10152 bos taurus
31	113.5	18.8	124	RNP_CAMDR P00670 camelus dno
32	113.5	18.8	128	RNP_HORSE P00674 equus caball
33	113	18.7	147	ANGI_HUMAN P03950 homo sapien

34	113	18.7	147	1	ANGI_PANTR	O8wn68 pan troglod
35	112.5	18.6	128	1	RNP_PROGU	P04059 proechimys
36	109.5	18.1	124	1	RNP_RANPA	P00666 rangifer ta
37	109.5	18.1	146	1	ANGI_PAPHA	O8wn64 papio hamad
38	109.5	18.1	148	1	RN14_MOUSE	O91jhl mus musculu
39	109	18.0	125	1	ANGI_RABIT	P31347 oryctolagus
40	108.5	17.9	124	1	RNP_CAPCA	P00664 capreolus c
41	108.5	17.9	124	1	RNP_GIRCA	P00662 giraffa cam
42	108.5	17.9	130	1	RNP_CITLO	P24717 citreululus
43	107.5	17.8	124	1	RNP_HUBBU	P00657 bubalus bub
44	107.5	17.8	148	1	RNP_PERLE	O9wnv5 peromyscus
45	107.5	17.8	149	1	RNP_ACOCA	O9wtls acomys calh

## ALIGNMENTS

RESULT 1  
ID RNPO\_RANCA STANDARD: PRT: 111 AA.  
AC P11916:  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding  
DE lectin) (SBL-C).  
OS Rana catesbeiana (Bull frog)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxId=8400;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Egg;  
RA MEDLINE=87299649; PubMed=3304421;  
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawachi H.,  
RA Takayanagi G., Hakomori S.;  
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana  
RT catesbeiana) eggs.";  
RT Biochemistry 26:2189-2194(1987).  
RN [2]  
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.  
RC MEDLINE=92220613; PubMed=1373237;  
RA Liao Y.-D.;  
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana  
RT catesbeiana (bullfrog) oocytes.";  
RT Nucleic Acids Res. 20:1371-1377(1992).  
RN [3]  
RP CHARACTERIZATION.  
RC TISSUE=Egg;  
RA MEDLINE=93192604; PubMed=8448385;  
RA Nitta K., Oyama F., Sekiguchi K., Kawachi H.,  
RA Takayanagi Y., Hakomori S., Titani K.;  
RT "Ribonuclease activity of sialic acid-binding lectin from Rana  
RT catesbeiana eggs.";  
RT Glycobiology 3:37-45(1993).  
RN [4]  
RP STRUCTURE BY NMR.  
RC MEDLINE=96437383; PubMed=9761686;  
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;  
RT "The solution structure of a cytochrome ribonuclease from the oocytes  
RT of Rana catesbeiana (bullfrog).";  
RT J. Mol. Biol. 283:231-244(1998).  
- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE  
RESIDUES WITH A 3'FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)  
AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS  
MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG  
EMBRYO. THIS LECTIN AGGLUTININATES VARIOUS ANIMAL CELLS, INCLUDING  
NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND  
HUMAN ORIGIN.  
- SUBUNIT: MONOMER.  
- SUBCELLULAR LOCATION: Secreted.  
- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
PIR: A27121; A27121.

PDB: 1BC4: 28-OCT-98.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC: 1.  
 KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure.  
 FT MOD\_RES 1 1 PIRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 71  
 FT DISULFID 34 81  
 FT DISULFID 52 96  
 FT DISULFID 93 110  
 SQ SEQUENCE 111 AA: 12464 MW: 0BC9E5F55729ECFA CRC64:

Query Match 96.8%; Score 585.5; DB 1; Length 111;  
 Best Local Similarity 97.3%; Pred. No. 9.5e-57;  
 Matches 108; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 2 QNMATFOOKHIINTPII-CNTILDNNIYVGGCKRVNTFTISSATYKATCGVILN 60  
 DB 1 QNMATFOOKHIINTPII-CNTILDNNIYVGGCKRVNTFTISSATYKATCGVILN 60  
 OY 61 LSTTRFQNLCTRTSTPRCPYSSRTETNYICVKCENQPVHFAIGRC 111  
 DB 61 LSTTRFQNLCTRTSTPRCPYSSRTETNYICVKCENQPVHFAIGRC 111

## RESULT 2

LECS\_RANJA STANDARD: PRT: 111 AA.  
 AC P18839:  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sialic acid-binding lectin (EC 3.1.27...)  
 OS Rana japonica (Japanese redbellied frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8402;  
 RN (1)  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC TISSUE-Egg;  
 RX MEDLINE=91035319; PubMed=2229005;  
 RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,  
 RA Takayanagi Y., Tlani K.;  
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)  
 RT eggs";  
 RT J. Biochem. 108:139-143(1990).  
 RL -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE  
 CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN  
 CC PREFERENTIALLY AGGLUTININATE A LARGE VARIETY OF TUMOR CELLS. BUT IT  
 CC DOES NOT AGGLUTININATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: JX0120; JX0120.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC: 1.  
 KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 72  
 FT DISULFID 34 82  
 FT DISULFID 52 97

FT DISULFID 94 111  
 SQ SEQUENCE 111 AA: 12326 MW: FDEBDE3834ED679 CRC64:

Query Match 74.5%; Score 451; DB 1; Length 111;  
 Best Local Similarity 77.5%; Pred. No. 3.6e-42;  
 Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;

OY 2 QNMATFOOKHIINTPII-CNTILDNNIYVGGCKRVNTFTISSATYKATCGVILN 59  
 DB 1 QNMATFOOKHIINTPII-CNTILDNNIYVGGCKRVNTFTISSATYKATCGVILN 59  
 OY 60 VLSTTRFQNLCTRTSTPRCPYSSRTETNYICVKCENQPVHFAIGRC 110  
 DB 61 VLSTTRFQNLCTRTSTPRCPYSSRTETNYICVKCENQPVHFAIGRC 111

## RESULT 3

RNPL\_RANJA STANDARD: PRT: 111 AA.  
 AC P14626:  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease, liver (EC 3.1.27.5).  
 OS Rana catesbeiana (bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN (1)  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=90130374; PubMed=2613682;  
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Matanabe H., Abe Y.,  
 RA Okazaki T., Ohgi K., Irie M.;  
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)  
 RT liver";  
 RT J. Biochem. 106:729-735(1989).  
 RL -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: JX0085; JX0085.  
 DR HSSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC: 1.  
 KW Hydrolase; Nuclease; Endonuclease.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 104 104  
 FT DISULFID 19 72  
 FT DISULFID 34 82  
 FT DISULFID 52 97  
 FT DISULFID 94 111  
 SQ SEQUENCE 111 AA: 12461 MW: D64BA72456C10788 CRC64:

Query Match 61.2%; Score 370; DB 1; Length 111;  
 Best Local Similarity 64.9%; Pred. No. 2.2e-33;  
 Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

OY 2 QNMATFOOKHIINTPII-CNTILDNNIYVGGCKRVNTFTISSATYKATCGVILN 59  
 DB 1 QNMATFOOKHIINTPII-CNTILDNNIYVGGCKRVNTFTISSATYKATCGVILN 59  
 OY 60 VLSTTRFQNLCTRTSTPRCPYSSRTETNYICVKCENQPVHFAIGRC 110  
 DB 61 VLSTTRFQNLCTRTSTPRCPYSSRTETNYICVKCENQPVHFAIGRC 111

RESULT 4  
 RN30\_RANPI STANDARD: PRT; 104 AA.  
 ID RN30\_RANPI  
 AC P22069;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE P-30 protein (EC 3.1.27.-) (Onconase).  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8434;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=91093131; PubMed=1985396;  
 RA Ardelt W., Mikulski S.M., Shogen K.;  
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens  
 oocytes and early embryos. Homology to pancreatic ribonucleases.";  
 RL J. Biol. Chem. 266:245-251(1991).  
 RN [2]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=93066156; PubMed=1438177;  
 RA Moslmann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.;  
 RA James M.N.G.;  
 RT "Comparative molecular modeling and crystallization of P-30 protein:  
 a novel antitumor protein of Rana pipiens oocytes and early  
 embryos.";  
 RL Proteins 14:392-400(1992).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RX MEDLINE=94160709; PubMed=8120892;  
 RA Moslmann S.C., Ardelt W., James M.N.G.;  
 RT "Refined 1.7 A x-ray crystallographic structure of P-30 protein, an  
 amphibian ribonuclease with anti-tumor activity.";  
 RL J. Mol. Biol. 236:1141-1153(1994).  
 CC -1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY  
 AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR  
 IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH  
 MOLECULAR WEIGHT RIBOSOMAL RNA.  
 CC MOLECULAR WEIGHT: 30 KDA.  
 CC -1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC PDB: 1ONC; 3I-TAN-94.  
 DR InterPro: IPR001427; Rnasea.  
 DR Pfam: PF00074; Rnasea: 1.  
 DR ProDom: PD000535; Rnasea: 1.  
 DR SMART: SM00092; Rnase\_Pc: 1.  
 DR PROSITE: PS00127; Rnase\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; 3D-structure.  
 FT MOD\_RES 1  
 FT ACT\_SITE 10  
 FT ACT\_SITE 31  
 FT ACT\_SITE 97  
 FT DISULFID 19  
 FT DISULFID 30  
 FT DISULFID 75  
 FT DISULFID 48  
 FT DISULFID 87  
 FT HELIX 3  
 FT HELIX 10  
 FT STRAND 11  
 FT STRAND 12  
 FT HELIX 19  
 FT TURN 22  
 FT TURN 24  
 FT TURN 26  
 FT STRAND 33  
 FT STRAND 38  
 FT HELIX 41  
 FT HELIX 48  
 FT TURN 49  
 FT TURN 50  
 FT STRAND 55  
 FT STRAND 58  
 FT STRAND 63  
 FT TURN 74  
 FT STRAND 77  
 FT STRAND 84  
 FT STRAND 86  
 FT TURN 92  
 FT TURN 93  
 FT STRAND 94  
 FT STRAND 101  
 SQ SEQUENCE 104 AA; 11845 MM; 22A753C2F9E56B4 CRC64;

Query Match 45.2% Score 273.5; DB 1; Length 104;  
 Best Local Similarity 48.6% Pred. No. 5.8e-23;  
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;  
 QY 2 QNNATPQOKHIIWT-PIICWTIIDNNIYIGQCKRVNTEFISSATVAKIGCVI-NLN 59  
 DQ 1 QDMLTFQKHIITNRVDVCNINSTNLF-----HKDKNTFIYSRPEVKAIKGIISKSN 56  
 QY 60 VLSTTRQLNTCTRTSTTPRCPYSSRTETNYICVKEENYVHFAIGRC 110  
 DQ 57 VLSTSEFVLSDC---NVTSPKCKYKIKKSTNKFVCEENAPVHFVGVGSC 104  
 RESULT 5  
 ID ANG3\_MOUSE STANDARD: PRT; 145 AA.  
 AC P97802;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)  
 DE (EF-5).  
 GN ANG3 OR ANGL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RX MEDLINE=97184476; PubMed=90322278;  
 RA Fu X., Kamps M.P.;  
 RT "E2a-Pbx1 induces aberrant expression of tissue-specific and  
 developmentally regulated genes when expressed in NIH 3T3  
 fibroblasts.";  
 RL Mol. Cell. Biol. 17:1503-1512(1997).  
 CC -1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 HYDROLYZING CELLULAR TRANS (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: U72672; AAC05794.1;  
 DR HSSP: P10152; IAGI.  
 DR MGD: MGI:1201793; Angl.  
 DR InterPro: IPR001427; Rnasea.  
 DR Pfam: PF00074; Rnasea: 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; Rnasea: 1.  
 DR SMART: SM00092; Rnase\_Pc: 1.  
 DR PROSITE: PS00127; Rnase\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 KW Protein synthesis inhibitor; Signal.  
 FT SIGNAL 1  
 FT CHAIN 25  
 FT MOD\_RES 25  
 FT ACT\_SITE 37  
 FT ACT\_SITE 64  
 FT ACT\_SITE 137  
 FT DISULFID 50  
 FT DISULFID 63  
 FT DISULFID 81  
 FT DISULFID 130  
 SQ SEQUENCE 145 AA; 16696 MM; DE9D3BC92F1D682C CRC64;





RESULT	ID	NAME	STANDARD	PRT	AA
10	RNBR_BOVIN				
AC	P39873				
DT	01-FEB-1995	(Rel. 31, created)			
DT	01-FEB-1995	(Rel. 31, last sequence update)			
DT	16-OCT-2001	(Rel. 40, last annotation update)			
DE	Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).				
GN	RN.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OX	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RP	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92093604; PubMed=1754384;				
RX	Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,				
RX	Viola M., Palmieri M., Russo E., Furia A.;				
RT	"Molecular cloning of the gene encoding the bovine brain ribonuclease				
RT	and its expression in different regions of the brain.";				
RL	Nucleic Acids Res. 19:6469-6474(1991).				
LN	[2]				
RP	SEQUENCE OF 27-167; AND CARBOHYDRATE-LINKAGE SITES.				
RP	TISSUE=Brain;				
RC	MEDLINE=89214015; PubMed=3243767;				
RX	Watanabe H., Katoh H., Ishii M., Komoda Y., Sando A., Takizawa Y.,				
RA	Ohki K., Irie M.,				
RT	"Primary structure of a ribonuclease from bovine brain.";				
RL	J. Biochem. 104:939-945(1988).				
LN	[3]				
RP	SEQUENCE OF 27-167 FROM N.A.				
RX	MEDLINE=96139017; PubMed=8587129;				
RA	Confalone E., Belmonte J.J., Sasso M.P., Carsana A., Palmieri M.,				
RA	Vento M.T., Furia A.;				
RT	"Molecular evolution of genes encoding ribonucleases in ruminant				
RT	species.";				
RT	J. Mol. Evol. 41:850-858(1995).				
LN	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL; X59767; CA442439.1; -				
DR	EMBL; S81744; AAB36138.1; -				
DR	PIR; S20066; S20066.				
DR	PIR; JX0056; JX0056.				
DR	HSSP; P00656; 2RNS.				
DR	GLYcositedb; P39873; -				
DR	InterPro: IPR001427; RNaseA.				
DR	Pfam; PF00074; RNaseA; 1.				
DR	PRINTS; PR00794; RIBONUCLEASE.				
DR	PRODOM; PD000535; RNaseA; 1.				
DR	SMART; SM00092; RNase_Pc; 1.				
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.				
DR	KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein; Signal.				
FT	SIGNAL	1	26		
FT	CHAIN	27	167		
FT	ACT_SITE	38			
FT	ACT_SITE	67			
FT	ACT_SITE	145			
FT	DISULFID	52	110		
FT	DISULFID	66	121		
FT	DISULFID	84	136		
FT	DISULFID	91	98		

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FT CARBOHYD 88 88 N-LINKED (GLUCANIC-...)/FTID=CAR_000005.
FT CARBOHYD 155 155 O-LINKED.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 T->S (IN REF. 2).
SQ SEQUENCE 167 AA: 18450 MW: 681CAAC3CC2FC459 CRC64;

Query Match: 21.4% Score 129.5; DB 1; Length 167;
Best Local Similarity 30.6% Pred. No. 3.9e-07;
Matches 37; Conservative 18; Mismatches 45; Indels 23; Gaps 7.

QY 5 ATFOOKHI-----INPILICNTLIDNNIYVGGQCKRVNTEFISSATTVKATGVNL 58
D 32 AKFRRQHHDDSSSSSNPNYCNQMMKKR-RMTHGCKRVNTEFVHESLDDVAVCS--QK 87
OY 59 NVL-----STTRFQNLNCTRTSTITPPR-CYSSRTETNYICVCE-NQY-PVIFA 105
D 88 NITCKNGHPNCQSKSTMSINDCRETSGSKYPNCAYKTSOKOKYITVACEGNPVYVHD 147
OY 106 G 106
D 148 C 148

RESULT 11
RNP_IGUIG
ID RNP_IGUIG STANDARD: PRT; 119 AA.
AC P80287;
D 01-FEB-1994 (Rel. 28, Created)
D 01-FEB-1994 (Rel. 28, Last sequence update)
D 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS Iguana iguana (Common Iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RL 11
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of Iguana (Iguana iguana) pancreatic
ribonuclease.";
Eut. J. Biochem. 219:641-646(1994).
CC -i- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- TISSUE SPECIFICITY: PANCREAS.
CC -i- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSSP; P00656; ILSO.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PRO0794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SMO0092; RNase.PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KM Hydroxylase; Nuclease; Endonuclease.
FT MOD_RS 1
FT DISULFID 25 80 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 39 91 BY SIMILARITY.
FT DISULFID 57 106 BY SIMILARITY.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
SQ SEQUENCE 119 AA: 13324 MW: 6072FB5B7B15BD5A CRC64;

Query Match: 21.1% Score 127.5; DB 1; Length 119;
Best Local Similarity 29.6% Pred. No. 4.5e-07;
Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps 4.

2 QNMATFOOKHI-----INPILICNTLIDNNIYVGGQCKRVNTEFISSATTVKATGVNL 52

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Db 1 QDMSFQNKHIDPETSASNPAYCDLMQOR-NLNPCKCTNTFVHASPSLQVCGS 59  
 OY 53 --TGVTINLNTSTRPOLNTCTRTST-PRCPYSSRTETNYCVGCENQYPVHF 104  
 Db 60 GGHYEDNLIDNSFIDLDCKNVGTAPSSCKYNGTPTGKRIRIACCENQPVHF 114

## RESULT 12

RNRB\_CARCA

ID RNRB\_CARCA STANDARD: PRT: 151 AA.

AC P79351;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
 OS Capreolus capreolus (Roe deer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;  
 OC Cervidae; Odocoileinae; Capreolus;  
 NCBI\_TaxID=9853;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98278842; PubMed=9611265;  
 RA Beukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,  
 RA Beukelman J.J.;  
 RL "Secretory ribonuclease genes and pseudogenes in true ruminants.";  
 RL Gene 212:259-268(1998).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: Y11673; CAA72371.1;  
 CC HSSP: P00656; ISRN.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA.1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR PRODOM: PD000535; RNaseA.1.  
 DR SMART: SM00092; RNase\_Pc.1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC.1.  
 DR KMHYDrolase; Nuclease; Endonuclease; Glycoprotein.  
 FT ACT\_SITE 41  
 FT DISULFID 26  
 FT DISULFID 40  
 FT DISULFID 58  
 FT DISULFID 65  
 FT CARBOHYD 125  
 FT CARBOHYD 133  
 FT CARBOHYD 133  
 SO SEQUENCE 151 AA; 16971 MW; 392D0E6302F06A6 CRC64;

Query Match 20.6%; Score 124.5; DB 1; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 1.2e-06;  
 Matches 34; Conservative 18; Mismatches 44; Indels 23; Gaps 6;

OY 5 AFPOQHITP-----ICNTILDNNTIYVGGCKRVNTFTIISATVKAICGVINL 58  
 ID RNRB\_CARCA STANDARD: PRT: 151 AA.  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RESULT 13  
 ANG2\_BOVIN  
 ID ANG2\_BOVIN STANDARD: PRT: 123 AA.  
 AC P80929;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin-2 (EC 3.1.27.-).  
 GN ANG2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Serum, and Milk;  
 RX MEDLINE=97409980; PubMed=9266695;  
 RA Stridom D.J., Bond M.D., Vallee B.L.;  
 RA "An angiogenic protein from bovine serum and milk -- purification and  
 RT primary structure of angiogenin-2".  
 RL Eur. J. Biochem. 247:535-544(1997).  
 CC -1- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND  
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC  
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
 CC HYDROLYZING CELLULAR TRNAS.

CC -1- TISSUE SPECIFICITY: SERUM, AND MILK.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR HSSP: P10152; IAGI.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA.1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR PRODOM: PD000535; RNaseA.1.  
 DR SMART: SM00092; RNase\_Pc.1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC.1.  
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
 KW Protein synthesis inhibitor; Glycoprotein;  
 KW MOD\_RRS 1  
 FT ACT\_SITE 12  
 FT ACT\_SITE 39  
 FT ACT\_SITE 113  
 FT DISULFID 25  
 FT DISULFID 38  
 FT DISULFID 91  
 FT CARBOHYD 56  
 FT CARBOHYD 106  
 FT CARBOHYD 33  
 SO SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 20.4%; Score 123.5; DB 1; Length 123;  
 Best Local Similarity 29.6%; Pred. No. 1.3e-06;  
 Matches 32; Conservative 20; Mismatches 43; Indels 13; Gaps 5;

OY 7 FQCKHIITPDI-----ICNTILDNNTIYVGGCKRVNTFTIISATVKAIC--TGVINL 58  
 ID RNRB\_CARCA STANDARD: PRT: 141 AA.  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RESULT 14  
 RNRB\_CARCA  
 ID RNRB\_CARCA STANDARD: PRT: 141 AA.  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.

